WHAT IS CLAIMED IS:

1. A substantially pure peptide which is capable of binding a PTB domain, wherein the peptide is from 5 to 100 amino acids in length, and comprises a core sequence of amino acids $NX_3X_1X_2X_4$;

wherein X_1 is selected from the group consisting of Y, pY or an analog thereof, E, T, D, Q, A and F;

X_2 is selected from pY or an analog thereof, and Y, provided that at least one of X_1 and X_2 is pY, or an analog thereof;

X_3 is selected from the group consisting of L and A; and

X_4 is selected from the group consisting of W, L, S, F and Q.

2. The peptide as recited in claim 1, wherein the peptide is from 6 to 100 amino acids in length, and comprises a core sequence of amino acids $X_5NX_3X_1X_2X_4$, wherein X_5 is selected from the group consisting of D, S, E and A.

3. The peptide as recited in claim 2, wherein X_2 is pY.

4. The peptide as recited in claim 3, wherein the peptide is from 6 to 100 amino acids in length, and comprises a core sequence of amino acids selected from the group consisting of $DNX_3X_1pYX_4$ and $ENX_3X_1pYX_4$, where X_4 is selected from the group consisting of W and F.

5. The peptide as recited in claim 2, wherein the peptide is from 12 to 100 amino acids in length, and comprises a core sequence of amino acids selected from the group consisting of AFDNLY(pY)WDQNS, AFDNL(pY)YWDQNS and AFDNL(pY)(pY)WDQNS.

6. The peptide as recited in claim 2, wherein the peptide is from 21 to 100 amino acids in length, and comprises

a core sequence of amino acids selected from the group consisting of: PAFSPAFDNLY(pY)WDQNSSEQG; PAFSPAFDNL(pY)YWDQNSSEQG; PAFSPAFDNL(pY)(pY)WDQNSSEQG; PAFSPAADNLY(pY)WDQNSSEQG; PAFSPAADNL(pY)YWDQNSSEQG; PAFSPAADNL(pY)(pY)WDQNSSEQG; PAFSPAFANLY(pY)WDQNSSEQG; PAFSPAFANL(pY)YWDQNSSEQG; PAFSPAFANL(pY)(pY)WDQNSSEQG; PAFSPAFSNLY(pY)WDQNSSEQG; PAFSPAFSNL(pY)YWDQNSSEQG; PAFSPAFSNL(pY)(pY)WDQNSSEQG; PAFSPAFDNAY(pY)WDQNSSEQG; PAFSPAFDNA(pY)YWDQNSSEQG; PAFSPAFDNA(pY)(pY)WDQNSSEQG; PAFSPAFDNLA(pY)WDQNSSEQG; PAFSPAFDNLF(pY)WDQNSSEQG; PAFSPAFDNLY(pY)FDQNSSEQG; PAFSPAFDNL(pY)YFDQNSSEQG; PAFSPAFDNL(pY)(pY)FDQNSSEQG; PAFSPAFDNLY(pY)WAQNSSEQG; PAFSPAFDNL(pY)YWAQNSSEQG; PAFSPAFDNL(pY)(pY)WAQNSSEQG; PAFSPAFDNLY(pY)WDANSSEQG; PAFSPAFDNL(pY)YWDANSSEQG; PAFSPAFDNL(pY)(pY)WDANSSEQG; PAFSPAFDNLY(pY)WDNNSSEQG; PAFSPAFDNL(pY)YWDNNSSEQG; PAFSPAFDNL(pY)(pY)WDNNSSEQG; PAFSPAFDNLY(pY)WDDNSSEQG; PAFSPAFDNL(pY)YWDDNSSEQG; PAFSPAFDNL(pY)(pY)WDDNSSEQG; PAFSPAFDNLY(pY)WDQASSEQG; PAFSPAFDNL(pY)YWDQASSEQG; PAFSPAFDNL(pY)(pY)WDQASSEQG; PAFSPAFDNLY(pY)WDQNASEQG; PAFSPAFDNL(pY)YWDQNASEQG; and PAFSPAFDNL(pY)(pY)WDQNASEQG.

7. The peptide as recited in claim 1, wherein at least one of X_1 and X_2 is an analog of phosphotyrosine, and said analog is (phosphonomethyl)phenylalanine.

8. A substantially pure peptide which is capable of binding a PTB domain, wherein the peptide is from 21 to about 100 amino acids in length and which comprises a core sequence of amino acids selected from the group consisting of AFGGAVENPE(pY)LAPRAGTASQ and EGTPTAENPE(pY)LGLDVPV.

9. A composition comprising a peptide as recited in claim 1, and a pharmaceutically acceptable carrier.

10. A method of determining whether a protein comprises a PTB domain, comprising the steps of:

contacting the protein with a peptide, which peptide is from 5 to 100 amino acids in length and comprises a core sequence of amino acids $NX_3X_1X_2X_4$, wherein X_1 is selected from the group consisting of Y, pY, E, T, D, Q, A and F; X_2 is selected from pY and Y, provided that at least one of X_1 and X_2 is pY; X_3 is selected from the group consisting of L and A; and X_4 is selected from the group consisting of W, L, S, F and Q; and

determining whether the peptide binds to the protein during said contacting step, where the binding of the peptide to the protein is indicative that the protein comprises a PTB domain.

11. The method as recited in claim 10, wherein prior to said contacting step, the protein is attached to a solid support;

the peptide used in said contacting step further comprises a detectable group fused to the peptide; and

said determining step comprises assaying for the presence of the detectable group.

12. The method as recited in claim 10, wherein prior to said contacting step, the peptide is attached to a solid support.

13. A method of determining whether a test compound is an agonist or antagonist of a PTB/phosphorylated ligand interaction, comprising the steps of:

incubating the test compound with a protein comprising a PTB domain and a peptide, which peptide is from 5 to 100 amino acids in length and which comprises a core amino acid sequence $NX_3X_1X_2X_4$, wherein X_1 is selected from the group consisting of Y, pY, E, T, D, Q, A and F; X_2 is selected from pY and Y, provided that at least one of X_1 and X_2 is pY; X_3 is selected from the group consisting of L and A; and X_4 is selected from the group consisting of W, L, S, F and Q; and

determining the amount of protein bound to the peptide during said incubating step; and

comparing the amount of protein bound to the peptide during said incubating step to an amount of protein bound to the peptide in the absence of the test compound, the increase or decrease in the amount of protein bound to the peptide in the presence of the test compound being indicative that the test compound is an agonist or antagonist of PTB domain/phosphorylated ligand interaction, respectively.

14. A method of inhibiting the binding of a PTB domain-containing protein to a tyrosine phosphorylated target, comprising contacting the PTB domain-containing protein with an effective amount of the peptide of claim 1.

15. The method as recited in claim 14, wherein the tyrosine phosphorylated target is c-erbB2.

16. The method as recited claim 15, wherein the PTB domain-containing protein is SHC.

17. A method of obtaining substantially pure PTB-domain-containing protein from a mixture of different proteins, comprising the steps of:

providing a peptide which is from 5 to 100 amino acids in length, and which comprises a core amino acid sequence $NX_3X_1X_2X_4$, wherein X_1 is selected from the group consisting of Y, pY, E, T, D, Q, A and F; X_2 is selected from pY and Y, provided that at least one of X_1 and X_2 is pY; X_3 is selected from the group consisting of L and A; and X_4 is selected from the group consisting of W, L, S, F and Q; bound to a solid support;

contacting the mixture of different proteins with the peptide bound to the solid support whereby the PTB domain-containing protein is bound to the peptide;

washing the solid support to remove unbound proteins; and

eluting substantially pure PTB-domain-containing protein from the solid support.

18. A method of treating a patient suffering from a proliferative cell disorder, comprising administering to the patient an effective amount of the peptide recited in claim 1.

19. The method as recited in claim 18, wherein the proliferative cell disorder is selected from the group consisting of atherosclerosis, inflammatory joint disease, psoriasis, restinosis and cancer.

20. The method as recited in claim 19, wherein the proliferative cell disorder is cancer.

21. The method as recited in claim 20, wherein the cancer is breast cancer.